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 FASTA searches a protein or DNA sequence data bank
 version 3.3t05 March 30, 2000
Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaKAARTa4pQ: 1093 aa
 >Lex 177 SEQ ID NO:4 human semaphorin
 vs  /tmp/fastaLAASTa4pQ library
searching /tmp/fastaLAASTa4pQ library

   1049 residues in     1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
 join: 39, opt: 27, gap-pen: -12/ -2, width:  16
 Scan time:  0.050
The best scores are:                                          opt
Lex 177 SEQ ID NO:2 human semaphorin
              (1049) 7485

>>Lex 177 SEQ ID NO:2 human semaphorin
                    (1049 aa)
 initn: 7483 init1: 7483 opt: 7485
Smith-Waterman score: 7485;  99.904% identity in 1043 aa overlap (51-1093:7-1049)

               30        40        50        60        70        80
Lex    SHLSSSQDVSSEPSSEQQLCALSKHPTVAFEDLQPWVSNFTYPGARDFSQLALDPSGNQL
                                    .:::::::::::::::::::::::::::::
Lex                                MTVVNPQDLQPWVSNFTYPGARDFSQLALDPSGNQL
                                           10        20        30

               90        100       110       120       130       140
Lex    IVGARNYLFRLSLANVSLLQATEWASSEDTRRSCQSKGKTEEECQNYVRVLIVAGRKVFM
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex    IVGARNYLFRLSLANVSLLQATEWASSEDTRRSCQSKGKTEEECQNYVRVLIVAGRKVFM
         40        50        60        70        80        90

              150       160       170       180       190       200
Lex    CGTNAFSPMCTSRQVGNLSRTIEKINGVARCPYDPRHNSTAVISSQGELYAATVIDFSGR
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex    CGTNAFSPMCTSRQVGNLSRTIEKINGVARCPYDPRHNSTAVISSQGELYAATVIDFSGR
        100       110       120       130       140       150

              210       220       230       240       250       260
Lex    DPAIYRSLGSGPPLRTAQYNSKWLNEPNFVAAYDIGLFAYFFLRENAVEHDCGRTVYSRV
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex    DPAIYRSLGSGPPLRTAQYNSKWLNEPNFVAAYDIGLFAYFFLRENAVEHDCGRTVYSRV
        160       170       180       190       200       210

              270       280       290       300       310       320
Lex    ARVCKNDVGGRFLLEDTWTTFMKARLNCSRPGEVPFYYNELQSAFHLPEQDLIYGVFTTN
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex    ARVCKNDVGGRFLLEDTWTTFMKARLNCSRPGEVPFYYNELQSAFHLPEQDLIYGVFTTN
        220       230       240       250       260       270

              330       340       350       360       370       380
Lex    VNSIAASAVCAFNLSAISQAFNGPFRYQENPRAAWLPIANPIPNFQCGTLPETGPNENLT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex    VNSIAASAVCAFNLSAISQAFNGPFRYQENPRAAWLPIANPIPNFQCGTLPETGPNENLT
        280       290       300       310       320       330
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            390       400       410       420       430       440
Lex     ERSLQDAQRLFLMSEAVQPVTPEPCVTQDSVRFSHLVVDLVQAKDTLYHVLYIGTESGTI
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex     ERSLQDAQRLFLMSEAVQPVTPEPCVTQDSVRFSHLVVDLVQAKDTLYHVLYIGTESGTI
         340       350       360       370       380       390

            450       460       470       480       490       500
Lex     LKALSTASRSLHGCYLEELHVLPPGRREPLRSLRILHSARALFVGLRDGVLRVPLERCAA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex     LKALSTASRSLHGCYLEELHVLPPGRREPLRSLRILHSARALFVGLRDGVLRVPLERCAA
         400       410       420       430       440       450

            510       520       530       540       550       560
Lex     YRSQGACLGARDPYCGWDGKQQRCSTLEDSSNMSLWTQNITACPVRNVTRDGGFGPWSPW
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex     YRSQGACLGARDPYCGWDGKQQRCSTLEDSSNMSLWTQNITACPVRNVTRDGGFGPWSPW
         460       470       480       490       500       510

            570       580       590       600       610       620
Lex     QPCEHLDGDNSGSCLCRARSCDSPRPRCGGLDCLGPAIHIANCSRNGAWTPWSSWALCST
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex     QPCEHLDGDNSGSCLCRARSCDSPRPRCGGLDCLGPAIHIANCSRNGAWTPWSSWALCST
         520       530       540       550       560       570

            630       640       650       660       670       680
Lex     SCGIGFQVRQRSCSNPAPRHGGRICVGKSREERFCNENTPCPVPIFWASWGSWSKCSSNC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex     SCGIGFQVRQRSCSNPAPRHGGRICVGKSREERFCNENTPCPVPIFWASWGSWSKCSSNC
         580       590       600       610       620       630

            690       700       710       720       730       740
Lex     GGGMQSRRRACENGNSCLGCGVEFKTCNPEGCPEVRRNTPWTPWLPVNVTQGGARQEQRF
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex     GGGMQSRRRACENGNSCLGCGVEFKTCNPEGCPEVRRNTPWTPWLPVNVTQGGARQEQRF
         640       650       660       670       680       690

            750       760       770       780       790       800
Lex     RFTCRAPLADPHGLQFGRRRTETRTCPADGSGSCDTDALVEDLLRSGSTSPHTVSGGWAA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex     RFTCRAPLADPHGLQFGRRRTETRTCPADGSGSCDTDALVEDLLRSGSTSPHTVSGGWAA
         700       710       720       730       740       750

            810       820       830       840       850       860
Lex     WGPWSSCSRDCELGFRVRKRTCTNPEPRNGGLPCVGDAAEYQDCNPQACPVRGAWSCWTS
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex     WGPWSSCSRDCELGFRVRKRTCTNPEPRNGGLPCVGDAAEYQDCNPQACPVRGAWSCWTS
         760       770       780       790       800       810

            870       880       890       900       910       920
Lex     WSPCSASCGGGHYQRTRSCTSPAPSPGEDICLGLHTEEALCATQACPEGWSPWSEWSKCT
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex     WSPCSASCGGGHYQRTRSCTSPAPSPGEDICLGLHTEEALCATQACPEGWSPWSEWSKCT
         820       830       840       850       860       870

            930       940       950       960       970       980
Lex     DDGAQSRSRHCEELLPGSSACAGNSSQSRPCPYSEIPVILPASSMEEATGCAGFNLIHLV
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex     DDGAQSRSRHCEELLPGSSACAGNSSQSRPCPYSEIPVILPASSMEEATGCAGFNLIHLV
         880       890       900       910       920       930
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               990       1000       1010       1020       1030       1040
Lex     ATGISCFLGSGLLTLAVYLSCQHCQRQSQESTLVHPATPNHLHYKGGGTPKNEKYTPMEF
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex     ATGISCFLGSGLLTLAVYLSCQHCQRQSQESTLVHPATPNHLHYKGGGTPKNEKYTPMEF
         940        950        960        970        980        990

              1050       1060       1070       1080       1090
Lex     KTLNKNNLIPDDRANFYPLQQTNVYTTTYYPSPLNKHSFRPEASPGQRCFPNS
        :::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex     KTLNKNNLIPDDRANFYPLQQTNVYTTTYYPSPLNKHSFRPEASPGQRCFPNS
        1000       1010       1020       1030       1040


1093 residues in 1 query   sequences
1049 residues in 1 library sequences
 Scomplib [version 3.3t05 March 30, 2000]
 start: Wed Oct 29 10:33:25 2003 done: Wed Oct 29 10:33:26 2003
 Scan time:  0.050 Display time:  1.567

Function used was FASTA
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